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               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004
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COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                 0.21       0.21

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FULL ESTIMATED COST	0.80	1.01

FILE 'CA' ENTERED AT 16:40:05 ON 23 NOV 2004

FILE 'MEDLINE' ENTERED AT 16:40:05 ON 23 NOV 2004

FILE 'BIOSIS' ENTERED AT 16:40:05 ON 23 NOV 2004

=> s archaeal polymerase
L1 4 ARCHAEAL POLYMERASE

=> d 1-4 ab, bib

L1 ANSWER 1 OF 4 CA COPYRIGHT 2004 ACS on STN
AB RNA polymerase from the hyperthermophile archaeon Pyrococcus furiosus (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochem. crosslinking method was used to map vicinity of the catalytic subunits of Pfu RNA polymerase to DNA locations distributed along the polymerase-promoter interface. The largest component of this **archaeal polymerase** is split into two subunits, A' and A'', whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homol. between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.
AN 134:142663 CA
TI The orientation of DNA in an archaeal transcription initiation complex
AU Bartlett, Michael S.; Thomm, Michael; Geiduschek, E. Peter
CS Department of Biology and Center for Molecular Genetics, University of California, La Jolla, CA, 92093-0634, USA
SO Nature Structural Biology (2000), 7(9), 782-785
CODEN: NSBIEW; ISSN: 1072-8368
PB Nature America Inc.
DT Journal
LA English
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L1 ANSWER 2 OF 4 MEDLINE on STN
AB RNA polymerase from the hyperthermophile archaeon Pyrococcus furiosus (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochemical crosslinking method was used to map the vicinity of the catalytic subunits of Pfu RNA polymerase to DNA

locations distributed along the polymerase-promoter interface. The largest component of this **archaeal polymerase** is split into two subunits, A' and A", whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homology between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.

AN 2000455673 MEDLINE
DN PubMed ID: 10966650
TI The orientation of DNA in an archaeal transcription initiation complex.
CM Comment in: Nat Struct Biol. 2000 Sep;7(9):703-5. PubMed ID: 10966630
AU Bartlett M S; Thomm M; Geiduschek E P
CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, California 92093-0634, USA.. bartlett@biomail.ucsd.edu
SO Nature structural biology, (2000 Sep) 7 (9) 782-5.
Journal code: 9421566. ISSN: 1072-8368.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Space Life Sciences
EM 200009
ED Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000928

L1 ANSWER 3 OF 4 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AB Deamination of cytosine to uracil in a G-C base pair is a major promutagenic event, generating G-CfwdarwA-T mutations if not repaired before DNA replication. Archaeal family B DNA polymerases are uniquely able to recognize unrepaired uracil in a template strand and stall polymerization upstream of the lesion, thereby preventing the irreversible fixation of an A-T mutation. We have now identified a 'pocket' in the N-terminal domains of archaeal DNA polymerases that is positioned to interact with the template strand and provide this ability. The structure of this pocket provides interacting groups that discriminate uracil from the four normal DNA bases (including thymine). These groups are conserved in **archaeal polymerase** but absent from homologous viral polymerases that are unable to recognize uracil. Using site-directed mutagenesis, we have confirmed the biological role of this pocket and have engineered specific mutations in the Pfu polymerase that confer the ability to read through template-strand uracils and carry out PCR with dUTP in place of dTTP.

AN 2003:81516 BIOSIS
DN PREV200300081516
TI Structural basis for uracil recognition by archaeal family B DNA polymerases.
AU Fogg, Mark J.; Pearl, Laurence H.; Connolly, Bernard A. [Reprint Author]
CS School of Cell and Molecular Biosciences, University of Newcastle, Newcastle upon Tyne, NE2 4HH, UK
b.a.connolly@ncl.ac.uk
SO Nature Structural Biology, (December 2002) Vol. 9, No. 12, pp. 922-927. print.
ISSN: 1072-8368 (ISSN print).
DT Article
LA English
ED Entered STN: 6 Feb 2003
Last Updated on STN: 6 Feb 2003

L1 ANSWER 4 OF 4 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AB RNA polymerase from the hyperthermophile archaeon Pyrococcus furiosus

(Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochemical crosslinking method was used to map the vicinity of the catalytic subunits of Pfu RNA polymerase to DNA locations distributed along the polymerase-promoter interface. The largest component of this **archaeal polymerase** is split into two subunits, A' and A", whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homology between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.

AN 2000:490391 BIOSIS
DN PREV200000490512
TI The orientation of DNA in an archaeal transcription initiation complex.
AU Bartlett, Michael S. [Reprint author]; Thomm, Michael; Geiduschek, E. Peter
CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, CA, 92093-0634, USA
SO Nature Structural Biology, (September, 2000) Vol. 7, No. 9, pp. 782-785. print.
ISSN: 1072-8368.
DT Article
LA English
ED Entered STN: 15 Nov 2000
Last Updated on STN: 10 Jan 2002